UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/048,116	02/27/2002	Nicolas Glaichenhaus	1721-47	6350

23117	7590	03/24/2006

NIXON & VANDERHYE, PC
901 NORTH GLEBE ROAD, 11TH FLOOR
ARLINGTON, VA 22203

EXAMINER
DIBRINO, MARIANNE NMN

ART UNIT	PAPER NUMBER
1644	

DATE MAILED: 03/24/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

10/048,116

APPLICATION NO./ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.

EXAMINER

ART UNIT	PAPER
1644	01232006

DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner for Patents

Please find below a communication from the EXAMINER in charge of this application

This application fails to comply with 37 C.F.R. 1.821-1.825 for the reason(s) listed on the Notice to comply with the sequence rules. The applicants are required to submit a new CRF and statement that the content of the paper and computer readable copies are the same, and where applicable, include no new matter.

37 C.F.R. 1.821 (e) A copy of the "Sequence Listing" referred to in paragraph © of this section must also be submitted in computer readable form in accordance with the requirements of § 1.824. The computer readable form is a copy of the "Sequence Listing" and will not necessarily be retained as part of the patent application file. If the computer readable form of a new application is to be identical with the computer readable form of another application of the applicant on file in the Office, reference may be made to the other application and computer readable form in lieu of filing a duplicate computer readable form in the new application. The new application shall be accompanied by a letter making such reference to the other application and computer readable form, both of which shall be completely identified.

(f) In addition to the paper copy required by paragraph © of this section and the computer readable form required by paragraph (e) of this section, a statement that the content of the paper and computer readable copies are the same must be submitted with the computer readable form. Such a statement must be a verified statement if made by a person not registered to practice before the Office.

Any inquiry concerning this communication should be directed to Examiner Marianne DiBrino, Art Unit 1644, whose telephone number is 571-272-0842.

APPLICANT IS GIVEN A ONE MONTH EXTENDABLE PERIOD WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Applicant is requested to return a copy of the attached Notice to Comply with the response.

Marianne DiBrino, Ph.D.

CHRISTINA CHAN
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

PTO-90C (Rev.04-03)

Application No.: 10/048,116

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth at 37 C.F.R. 1.821 - 1.825 for the following reason(s):

_____X__1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

_____2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

_____3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

____X___4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

_____5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

_____6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

_____7. Other:

Applicant Must Provide:

___X___A substitute computer readable form (CRF) copy of the "Sequence Listing".

___X__A substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

___X__A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:
For Rules Interpretation, call   (703) 308-4216
For CRF Submission Help, call   (703) 308-421
PatentIn Software Program Support (SIRA)
    Technical Assistance...........................703-287-0200
    To Purchase PatentIn Software...........703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information. Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/048,116A_

Source: _1FwJ/6_

Date Processed by STIC: _12/29/05_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
> http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building. 401 Dulany Street. Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: *10/048,116A*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
    Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
    prevent "wrapping."

2____Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
    Numbering   use space characters, instead.

4____Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
    ensure your subsequent submission is saved in ASCII text.

5____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules,
    each n or Xaa can only represent a single residue. Please present the maximum number of each
    residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_✓_PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
    "bug"   sequences(s) _2,4,6,8_. Normally, PatentIn would automatically generate this section from the
    previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
    the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
    Artificial or Unknown sequences.

7____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
    , (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
    (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
    This sequence is intentionally skipped

    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
   (NEW RULES)   <210> sequence id number
    <400> sequence id number
    000

9____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
    (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
    Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
    is Artificial Sequence

11____Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
    "Unknown." Please explain source of genetic material in <220> to <223> section.
    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
    "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
    listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n/Xaa   "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003
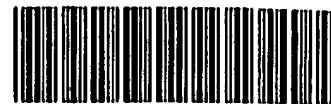
IFW16

RAW SEQUENCE LISTING   DATE: 12/29/2005
PATENT APPLICATION: US/10/048,116A   TIME: 12:20:15

Input Set : A:\seq list.txt
Output Set: N:\CRF4\12292005\J048116A.raw

```
 3 <110> APPLICANT: CNRS
 5 <120> TITLE OF INVENTION: RECOMBINANT PROTEINS AND MOLECULAR COMPLEXES DERIVED
 6       FROM THESE PROTEINS, ANALOGOUS TO MOLECULES INVOLVED IN
 7       IMMUNE RESPONSES
 9 <130> FILE REFERENCE: 1721-47
11 <140> CURRENT APPLICATION NUMBER: 10/048,116A
12 <141> CURRENT FILING DATE: 2002-02-27
14 <150> PRIOR APPLICATION NUMBER: PCT/FR00/02193
15 <151> PRIOR FILING DATE: 2000-07-28
17 <150> PRIOR APPLICATION NUMBER: FR99/09862
18 <151> PRIOR FILING DATE: 1999-07-29
20 <160> NUMBER OF SEQ ID NOS: 8
22 <170> SOFTWARE: PatentIn Ver. 2.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1517
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Description of Artificial Sequence: construct
31       coding IAalpha(d)/Fc
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (18)..(1502)
37 <400> SEQUENCE: 1
38 aaagggggga attcagg atg ccg tgc agc aga gct ctg att ctg ggg gtc     50
39                     Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val
40                      1               5                  10
42 ctc gcc ctg aac acc atg ctc agc ctc tgc gga ggt gaa gac gac att    98
43 Leu Ala Leu Asn Thr Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile
44          15                  20                  25
46 gag gcc gac cac gta ggc ttc tat ggt aca act gtt tat cag tct cct   146
47 Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro
48          30                  35                  40
50 gga gac att ggc cag tac aca cat gaa ttt gat ggt gat gag ttg ttc   194
51 Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe
52      45                  50                  55
54 tat gtg gac ttg gat aag aag aaa act gtc tgg agg ctt cct gag ttt   242
55 Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe
56  60                  65                  70                  75
58 ggc caa ttg ata ctc ttt gag ccc caa ggt gga ctg caa aac ata gct   290
59 Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala
60                  80                  85                  90
62 gca gaa aaa cac aac ttg gga atc ttg act aag agg tca aat ttc acc   338
```

```
63 Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr
64          95              100             105
66 cca gct acc aat gag gct cct caa gcg act gtg ttc ccc aag tcc cct   386
67 Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro
68          110             115             120
70 gtg ctg ctg ggt cag ccc aac acc ctt atc tgc ttt gtg gac aac atc   434
71 Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile
72      125             130             135
74 ttc cca cct gtg atc aac atc aca tgg ctc aga aat agc aag tca gtc   482
75 Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val
76 140             145             150             155
78 aca gac ggc gtt tat gag acc agc ttc ctc gtc aac cgt gac cat tcc   530
79 Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser
80              160             165             170
82 ttc cac aag ctg tct tat ctc acc ttc atc cct tct gat gat gac att   578
83 Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile
84          175             180             185
86 tat gac tgc aag gtg gag cac tgg ggc ctg gag gag ccg gtt ctg aaa   626
87 Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys
88          190             195             200
90 cac tgg gaa cct gag att cca gcc ccc atg tca gag ctg aca gaa act   674
91 His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr
92      205             210             215
94 gga ggt gga gga tcc act aca gct cca tca gct cag ctc gaa aaa gag   722
95 Gly Gly Gly Gly Ser Thr Thr Ala Pro Ser Ala Gln Leu Glu Lys Glu
96 220             225             230             235
98 ctc cag gcc ctg gag aag gaa aat gca cag ctg gaa tgg gag ttg caa   770
99 Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln Leu Glu Trp Glu Leu Gln
100             240             245             250
102 gca ctg gaa aag gaa ctg gct cag gca gca tct gag ccc aga ggg ccc  818
103 Ala Leu Glu Lys Glu Leu Ala Gln Ala Ala Ser Glu Pro Arg Gly Pro
104             255             260             265
106 aca atc aag ccc tgt cct cca tgc aaa tgc cca gca cct aac ctc ttg  866
107 Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu
108             270             275             280
110 ggt gga cca tcc gtc ttc atc ttc cct cca aag atc aag gat gta ctc  914
111 Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu
112     285             290             295
114 atg atc tcc ctg agc ccc ata gtc aca tgt gtg gtg gtg gat gtg agc  962
115 Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser
116 300             305             310             315
118 gag gat gac cca gat gtc cag atc agc tgg ttt gtg aac aac gtg gaa  1010
119 Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu
120             320             325             330
122 gta cac aca gct cag aca caa acc cat aga gag gat tac aac agt act  1058
123 Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr
124             335             340             345
126 ctc cgg gtg gtc agt gcc ctc ccc atc cag cac cag gac tgg atg agt  1106
127 Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser
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RAW SEQUENCE LISTING   DATE: 12/29/2005
PATENT APPLICATION: US/10/048,116A   TIME: 12:20:15

Input Set : A:\seq list.txt
Output Set: N:\CRF4\12292005\J048116A.raw

```
128        350              355              360
130 ggc aag gag ttc aaa tgc aag gtc aac aac aaa gac ctc cca gcg ccc    1154
131 Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro
132     365              370              375
134 atc gag aga acc atc tca aaa ccc aaa ggg tca gta aga gct cca cag    1202
135 Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln
136 380              385              390              395
138 gta tat gtc ttg cct cca cca gaa gaa gag atg act aag aaa cag gtc    1250
139 Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val
140              400              405              410
142 act ctg acc tgc atg gtc aca gac ttc atg cct gaa gac att tac gtg    1298
143 Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val
144     415              420              425
146 gag tgg acc aac aac ggg aaa aca gag cta aac tac aag aac act gaa    1346
147 Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu
148     430              435              440
150 cca gtc ctg gac tct gat ggt tct tac ttc atg tac agc aag ctg aga    1394
151 Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg
152     445              450              455
154 gtg gaa aag aag aac tgg gtg gaa aga aat agc tac tcc tgt tca gtg    1442
155 Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val
156 460              465              470              475
158 gtc cac gag ggt ctg cac aat cac cac acg act aag agc ttc tcc cgg    1490
159 Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg
160              480              485              490
162 act ccg ggt aaa tgatgactcg acctg                                   1517
163 Thr Pro Gly Lys
164              495
167 <210> SEQ ID NO: 2
168 <211> LENGTH: 495
169 <212> TYPE: PRT
170 <213> ORGANISM: Artificial Sequence
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W--> 172 <220> FEATURE:
W--> 172 <223> OTHER INFORMATION: *see item 6 on Erro Summary Sheet*
W--> 172 <400> 2

(same error in seqs. 4, 6, 8)

```
173 Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val Leu Ala Leu Asn Thr
174  1           5              10              15
176 Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val
177          20              25              30
179 Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln
180          35              40              45
182 Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp
183     50              55              60
185 Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu
186  65              70              75              80
188 Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn
189          85              90              95
191 Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu
192          100             105             110
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RAW SEQUENCE LISTING   DATE: 12/29/2005
PATENT APPLICATION: US/10/048,116A   TIME: 12:20:15

Input Set : A:\seq list.txt
Output Set: N:\CRF4\12292005\J048116A.raw

```
194 Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln
195         115             120             125
197 Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile
198         130             135             140
200 Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr
201 145             150             155             160
203 Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser
204         165             170             175
206 Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val
207         180             185             190
209 Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu
210         195             200             205
212 Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr Gly Gly Gly Gly Ser
213         210             215             220
215 Thr Thr Ala Pro Ser Ala Gln Leu Glu Lys Glu Leu Gln Ala Leu Glu
216 225             230             235             240
218 Lys Glu Asn Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu
219         245             250             255
221 Leu Ala Gln Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys
222         260             265             270
224 Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val
225         275             280             285
227 Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser
228         290             295             300
230 Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp
231 305             310             315             320
233 Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln
234         325             330             335
236 Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser
237         340             345             350
239 Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys
240         355             360             365
242 Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile
243         370             375             380
245 Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro
246 385             390             395             400
248 Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met
249         405             410             415
251 Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn
252         420             425             430
254 Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser
255         435             440             445
257 Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn
258         450             455             460
260 Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu
261 465             470             475             480
263 His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
264         485             490             495
267 <210> SEQ ID NO: 3
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RAW SEQUENCE LISTING   DATE: 12/29/2005
PATENT APPLICATION: US/10/048,116A   TIME: 12:20:15

Input Set : A:\seq list.txt
Output Set: N:\CRF4\12292005\J048116A.raw

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268 <211> LENGTH: 1485
269 <212> TYPE: DNA
270 <213> ORGANISM: Artificial Sequence
272 <220> FEATURE:
273 <223> OTHER INFORMATION: Description of Artificial Sequence:coding region
274       of SEQ ID NO:1
276 <220> FEATURE:
277 <221> NAME/KEY: CDS
278 <222> LOCATION: (1)..(1485)
280 <400> SEQUENCE: 3
281 atg ccg tgc agc aga gct ctg att ctg ggg gtc ctc gcc ctg aac acc    48
282 Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val Leu Ala Leu Asn Thr
283  1               5                  10                  15
285 atg ctc agc ctc tgc gga ggt gaa gac gac att gag gcc gac cac gta    96
286 Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val
287              20                  25                  30
289 ggc ttc tat ggt aca act gtt tat cag tct cct gga gac att ggc cag   144
290 Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln
291          35                  40                  45
293 tac aca cat gaa ttt gat ggt gat gag ttg ttc tat gtg gac ttg gat   192
294 Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp
295      50                  55                  60
297 aag aag aaa act gtc tgg agg ctt cct gag ttt ggc caa ttg ata ctc   240
298 Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu
299 65                  70                  75                  80
301 ttt gag ccc caa ggt gga ctg caa aac ata gct gca gaa aaa cac aac   288
302 Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn
303              85                  90                  95
305 ttg gga atc ttg act aag agg tca aat ttc acc cca gct acc aat gag   336
306 Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu
307             100                 105                 110
309 gct cct caa gcg act gtg ttc ccc aag tcc cct gtg ctg ctg ggt cag   384
310 Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln
311         115                 120                 125
313 ccc aac acc ctt atc tgc ttt gtg gac aac atc ttc cca cct gtg atc   432
314 Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile
315     130                 135                 140
317 aac atc aca tgg ctc aga aat agc aag tca gtc aca gac ggc gtt tat   480
318 Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr
319 145                 150                 155                 160
321 gag acc agc ttc ctc gtc aac cgt gac cat tcc ttc cac aag ctg tct   528
322 Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser
323             165                 170                 175
325 tat ctc acc ttc atc cct tct gat gat gac att tat gac tgc aag gtg   576
326 Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val
327         180                 185                 190
329 gag cac tgg ggc ctg gag gag ccg gtt ctg aaa cac tgg gaa cct gag   624
330 Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu
331         195                 200                 205
```

Input Set : **A:\seq list.txt**
Output Set: **N:\CRF4\12292005\J048116A.raw**

L:172 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:2, <213>
ORGANISM:Artificial Sequence
L:172 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>
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ORGANISM:Artificial Sequence
L:768 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:768